1632

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/458,366A

DATE: 01/04/2001 TIME: 13:03:43

Input Set : A:\ES.txt
Output Set: N:\CRF3\01042001\1458366A.raw





	•		
	<110> APPLICANT: Evans, Rona	ald M.	•
5			The safe
7	· ·	OVEL STEROID-ACTIVATED NUCLEAR	
8		REFOR -	ENTERED
	<130> FILE REFERENCE: SALK22	270-2	
	<140> CURRENT APPLICATION NU	PRODUCT 0 77 430 7 30 0 A	
	<141> CURRENT FILING DATE: 1		
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	<151> PRIOR FILING DATE: 199		
	<160> NUMBER OF SEQ ID NOS:		
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	<220> FEATURE:	•	TIVED
	<221> NAME/KEY: CDS		
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	<400> SEQUENCE: 1	s selected from A, C, 1/0 of G	JAN 0 8 2001
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		agac ctgaaagaaa aaagtaggga gaacataatg	180 TECH CENTER 1600/2900
		tgot agttcaagtg otggacttgg gacttaggag	240
	3.	eatct gacttggact gaaatatagg tgagagacaa	300
		aacc tatgactagg acgygaagag gaagcactge	360
	*	cago otgoaayooa aytyttoaca gtgagaaaag	420
		ectga acaaggeage ggeteettgg taaagetaet	480
	3 5 5	gttc amagtggacc ccaggggaga agtcggagca	540
	2 2 2 2	agge ecagaageaa ac etg gag gtg aga	594
44		Leu Glu Val Arg	
45		1	
47	ecc aaa qaa age tgg aac cat	get gae tit gia cae tgt gag gae aca	642
		Ala Asp Phe Val His Cys Glu Asp Thr	
49		15 . 20	
51	gag tot gtt oot gga aag ooc	agt gtc aac gca gat gag gaa gtc gga	690
52	Glu Ser Val Pro Gly Lys Pro	Ser Val Asn Ala Asp Glu Glu Val Gly	
53	25	30 35	
		tgt ggg gac aag gcc act ggc tat cac	738
56	Gly Pro Gln Ile Cys Arg Val	Cys Gly Asp Lys Ala Thr Gly Tyr His	
57		45 50	
		gga tgc aag ggc ttt ttc agg agg gcc	786
		Gly Cys Lys Gly Phe Phe Arg Arg Ala	•
61	55	60 65	
		agg tgc ccc ttc cgg aag ggc gcc tgc	834
		Arg Cys.Pro Phe Arg Lys Gly Ala Cys	•
65	70 . 75	80 .	

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	67	gag	atc	acc	cqg	aag	acc	cgg	cga	cag	tgc	cag	gcc	tgc	cgc	ctg	cgc	882
	68	Glu	$_{\rm Ilc}$	Thr	Arg	Lys	Thr	Arg	Arg	Gln	Cys	Gln	Al.a	Cys	Arg	Leu	Arg	
	69	85					90					95					100	
	7.1	aag	tgc	ctg	gag	agc	ggc	atg	aag	aaq	gag	atq	atc	atg	tcc	gac	gag	930
	72	Lys	Cys	Leu	Glu	Ser	Gly	Иet	Lys	Lys	Glu	Иet	I l.e	Met	ser	Asp	Glu	
	73					105					110					115		
	75	oup.	gtg	gag	qag	agg	cgg	gcc	ttg	atc	aag	cgg	aag	aaa	agt	gaa	cgq	978
	76	Ala	Val	Glu	Glu	Arg	Arg	Ala	Leu	Lle	Lys	Arg	Lys	Lys	ser	Glu	Arg	
	77				1.20					125					130			
	79	aca	gġg	act	cag	cca	ctg	gga	gtg	cag	ggg	ctg	aca	gag	gag	cag	cgg	1026
	30	Thr	Gly	Thr	Gln	Pro	Leu	Gly	Val	G1n	Gly	Leu	Thr	Glu	Glu	Gln	Arg	
	81			135					140					1.45				
	8.3	atg	atg	atc	agg	gag	ctg	atq	gac	get	cag	atg	aaa	acc	ttt	gae	act	1074
	84	Met	Met	Tle	Arg	Glu	Leu	Met	Asp	Ala	Gin	Met	Lys	Thr	Phe	Asp	Thr	
	85		150					155					160					
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	88	Thr	Phe	Ser	His	Phe	$L\gamma s$	Asn	Phe	Arg	Leu	Pro	Gly	Val	Leu	ser	Ser	
	89	1.65					170					175					180	
	91	ggc	tgc	gag	t.t.g	cca	gag	cet	ctg	cag	gcc	cca	t.cg	agg	gaa	gaa	get.	1170
	92	Gly	Cys	Glu	Leu	Pro	Glu	Pro	Leu	Gln	Ala	Pro	Ser	Arg	Glu	Glu	Ala	
	93					185					190.					195		
	95	gcc	aag	t.gg	agc	cag	gtc	egg	aaa	gat:	ctg	tgc	tct	ttg	aag	gtc	tet	1218
	96	Ala	Lys	Trp	Ser	G.l.n	Va l.	Arg	Lys	Asp	Leu	Cys	Ser	Leu	Lys	Val	ser	
	97				200					205					210			
W>	99	ctg	caa	gct	aca	aaa	ααa	ααa	t.aa	cad	tat	cta	maa	cta	caa	acn	ccc	1266
								J 3	~ 5 5	~ ~ 9	cy c		gau	CCu	ouu	4011		~=
M>	100	Leu	Glr	Ala													Pro	
W>	100		Glr	215	Ala					Gln					Glr			
W>	101			215	Ala	Gly	G1y	Gly	Trp 220	Gln	Cys	Leu	Glu	Leu 225	Glr	xaa		1314
W>	101 103	ago	e ega	215 cag	Ala tgg	Gly	Gly aaa	Gly gag	Trp 220 ato	Gln ttc	cys tcc	Leu ctg	Glu ctg	Leu 225 ccc	Glr cac	xaa atg	Pro	
W>	101 103	agc Se.r	e ega	215 cag Gln	Ala tgg	Gly	Gly aaa	Gly gag	Trp 220 ato	Gln ttc	cys tcc	Leu ctg	Glu ctg	Leu 225 ccc Pro	Glr cac	xaa atg	Pro gct	
W>	101 103 104 105	agc Se.r	e ega Arg 230	215 cag Gln	tgg Trp	Gly cgg Arg	Gly aaa Lys	gag Glu 235	Trp 220 ato 1116	tto Phe	tco Ser	Leu ctg	Glu ctg Leu 240	Leu 225 ecc Pro	cac His	xaa atg Met	Pro gct	
W>	101 103 104 105	agc Ser	c cga Arg 230 atg	215 cag Gln tca	tgg Trp	Gly cgg Arg	aaa Lys atg	gag Glu 235	Trp 220 ato 111e aaa	tto Phe	cys tcc ser atc	Leu ctg Leu atc	Glu ctg Leu 240 ago	Leu 225 ccc Pro	cac His	xaa atg Met	Pro gct Ala	1314
W>	101 103 104 105 107 108	agc Ser	c cga Arg 230 atg	215 cag Gln tca	tgg Trp	Gly cgg Arg	aaa Lys atg	gag Glu 235 ttc	Trp 220 ato 111e aaa	tto Phe	cys tcc ser atc	Leu ctg Leu atc	ctg Leu 240 ago	Leu 225 ccc Pro	cac His	xaa atg Met	Pro gct Ala gtc	1314
W>	101 103 104 105 107 108 109	gac Ser gac Asp 245	c cga c Arg 230 c atg Met	215 cag Glm tca tca Ser	tgg Trp	Gly Ggg Arg tac Tyr	Gly aaa Lys atg Met 250 gac	gag Glu 235 tto Phe	Try 220 ato 1116 aaaa Lys	e tto Phe ggo Gly	tcc server atc	teu ctg	Glu ctg Leu 240 agc Ser cag	Leu 225 ccc Pro tttt Phe	Glr cac His gcc Ala	Xaa Atg Met aaa Lys ctg	Pro got Ala gtc Val 260 ctg	1314
W>	101 103 104 105 107 108 109	gac Ser gac Asp 245	c cga c Arg 230 c atg Met	215 cag Glm tca tca Ser	tgg Trp	Gly Ggg Arg tac Tyr	Gly aaa Lys atg Met 250 gac	gag Glu 235 tto Phe	Try 220 ato 1116 aaaa Lys	e tto Phe ggo Gly	tcc server atc	teu ctg	Glu ctg Leu 240 agc Ser cag	Leu 225 ccc Pro tttt Phe	Glr cac His gcc Ala	Xaa Atg Met aaa Lys ctg	gct Ala gtc Val 260	1314
W>	101 103 104 105 107 108 109	gac Asp 245	c cga c Arg 230 c atg Met	215 cag Glm tca tca Ser	tgg Trp acc	Gly Ggg Arg tac Tyr	aaa Lys atg Met 250 gac Asp	gag Glu 235 tto Phe	Try 220 ato 116 aaa baaa bys	e tto Phe ggo Gly	tcc server atc	Leu ctg Leu atc atc 255 gac Asp	Glu ctg Leu 240 agc Ser cag	Leu 225 ccc Pro tttt Phe	Glr cac His gcc Ala	Xaa Atg Met aaa Lys ctg	Pro gct Ala gtc Val 260 ctg	1314
W>	101 103 104 105 107 108 109 111 112	gac Asp 245	c cga 230 atg Met tcc Ser	215 cag Glm tea Ser tac	tgg Trp acc Thr	Gly Ggg Arg tac Tyr Arg Arg	aaa Lys atg Met 250 gac Asp	gag Glu 235 tto Phe ttg	Tri 220 ato 116 aaa Lys coo	e tto Phe ggo Gly ato	cys control co	ctg Leu atc atc 1le 255 gac Asp	otg teu 240 ago ser cag	Leu 225 ccc Pro tttt Phe atc	Glr cac His gcc Ala tcc	xaa c atg Met c aaaa Lys ctg Leu 275	Pro gct Ala gtc Val 260 ctg	1314
W>	101 103 104 105 107 108 109 111 112 113	gac Ser gac Asp 245 atc	c oga c Arg 230 c atg Met c too	215 cag Glm tea Ser tac Tyr	tgg Trp acc Thr ttc Phe	Gly Cgg Arg tac Tyr agg Arg Arg	aaaa Lys atg Met 250 gac Asp	gag Glu 235 tto Phe ttg	Tri 220 ato Ile aaaa Lys coo Pro	e ttc Phe ggc Gly atc	tco Ser atc Ile gag Glu 270 ctg	Leu ctg Leu catc atc 255 gac Asp	Glu ctg Leu 240 agc Ser cag Gln	Leu 225 ccc Pro	Glr cac His gcc Ala tcc Ser	xaa c atg Met c aaa Lys c ctg Leu 275	Pro gct Ala gtc Val 260 ctg	1314 1362 1410
W>	101 103 104 105 107 108 109 111 112 113	ago Ser gao Asp 245 ato Lie	c oga c Arg 230 c atg Met c too	215 cag Glm tea Ser tac Tyr	tgg Trp acc Thr	Gly Ggg Arg tac Tyr Arg Arg Arg	aaaa Lys atg Met 250 gac Asp	gag Glu 235 tto Phe ttg	Tri 220 ato Ile aaaa Lys coo Pro	e ttc Phe ggc Gly atc	tcc Ser atc Ile gag Glu 270 ctg	Leu ctg Leu catc atc 255 gac Asp	Glu ctg Leu 240 agc Ser cag Gln	Leu 225 ccc Pro	Glr cac His gcc Ala tcc Ser	xaa a atg Met aaaa Lys ctg Leu 275 gtg	Pro gct Ala gtc Val 260 ctg Leu	1314 1362 1410
W>	101 103 104 105 107 108 109 111 112 113 115 116	gac Asp 245 atc 11e	c cga 230 c atg Met c tcc ser ggg	215 cag Glm tea Ser tac Tyr	tgg Trp acc Thr ttc Phe gct Ala 280	Gly Ggg Arg tac Tyr agg Arg 265	aaaa Lys atg Met 250 gac Asp	gag Glu 235 tto Phe ttg Leu	Trr 22(atc 11e aaa Lys Cod Pro	e tto Phe ggo Gly ato Ile caa	tec Ser atc Ile gag Glu 270 ctg	c teu c teu c ato c ato c ato 255 gao a Asp	Glu Ctg Leu 240 agc Ser Cag Gln ttc	Leu 225 COCC Pro	Glr cac His GC Ala tcc Ser aca Thr 290	a Xaa a atg a Met a aaa Lys c ctg Leu 275 g tgtg	Pro gct Ala gtc Val 260 ctg Leu	1314 1362 1410
W>	101 103 104 105 107 108 109 111 112 113 115 116 117	ago Ser gao Asp 245 ato Lie aag	c cga c Arg 230 c atg met c too Ser ggg	215 cag Glm tea Ser tac Tyr Gcc Ala	Ala tgg Trp acc Thr ttc Phe gct Ala 280	Gly Ggg Arg tac Tyr Arg 265 ttc	aaaa Lys atg Met 250 gac Asp Glu	gag gag glu 235 tto Phe ttg	Tri 22(atc life aas Lys cod Pro	e tto Phe ggc Gly atc Ile caa Gln 285	tec Ser atc Ile gag Glu 270 ctg Leu	E Leu c otg c atc c atc 255 gac Asp aga Arg	Glu ctg teu 240 agc ser cagg cagg cagg chatte	Leu 225 ccc Pro	Glr cac His GC Ala tcc Ser aca Thr 290 tac	xaa e atg Met aaaa Lys ctg 275 gtg val	gct Ala gtc Val 260 ctg Leu	1314 1362 1410 1458
W>	101 103 104 105 107 108 109 111 112 113 115 116 117	ago Ser gao Asp 245 ato Lie aag	c cga c Arg 230 c atg met c too Ser ggg	215 cag Glm tea Ser tac Tyr Gcc Ala	Ala tgg Trp acc Thr ttc Phe gct Ala 280 act	Gly Ggg Arg tac Tyr Arg 265 ttc	aaaa Lys atg Met 250 gac Asp Glu	gag gag glu 235 tto Phe ttg	Tri 22(atc life aas Lys cod Pro	e tto Phe ggc Gly atc Ile caa Gln 285 tgt	tec Ser atc Ile gag Glu 270 ctg Leu	E Leu c otg c atc c atc 255 gac Asp aga Arg	Glu ctg teu 240 agc ser cagg cagg cagg chatte	Leu 225 ccc Pro	Glr cac His GC Ala tcc Ser aca Thr 290 tac	xaa e atg Met aaaa Lys ctg 275 gtg val	gct. Ala gtc: Val 260 ctg Leu ttc. Phe	1314 1362 1410 1458
W>	101 103 104 105 107 108 109 111 112 113 115 116 117 119 120 121	ago Ser gac Asp 245 ato Lie aag Lys	c cga c Arg 230 atg Met c tcc Ser ggg Gly	215 cag Glm tea Ser tac Tyr gcc Ala gag Glu 295	tigg Trp acc Thr ttc Phe gct Ala 280 act	Gly cgg Arg tac Tyr agg Arg 265 ttc Phe	aaaa Lys atg Met 250 gac Asp Glu acc	gag Glu 235 tto Phe ttg Leu	Try 220 atc 116 aaaa Lys ccc Pro tgt Cys	e tto Phe ggc Gly atc Ile caa Gln 285 tgt	cys tec Ser atc atc Ile gag Glu 270 ctg Leu	E Leu c atc c atc c atc c atc c Asp d aga Arg c Arg	ctg 240 ago Ser cago Gln tto Phe ctg	Leu 225 ccc Pro	Glr cac His GC Ala tcc Ser aca Thr 290 tac	xaa a atg Met aaaa Lys ctg 275 gtg Val	gct. Ala gtc: Val 260 ctg Leu ttc. Phe	1314 1362 1410 1458
W>	1011 103 104 105 107 108 109 111 112 113 115 116 117 119 120 121 123 124	gac Asp 245 atc 11e agg Lys ac Asp	c cga c Arg 230 c atg c Met c tcc c Ser c Gly c Gly c Ala	215 cag Glm	Ala tgg Trp acc Thr ttc Phe Ala 280 act Thr	Gly cgg Arg tac Tyr agg Arg 265 ttc Phe gga Gly	Gly aaa Lys atg Met 250 gac Asp Glu acc Thr	gagger ga	Try 220 atcc 11e accc 12e cocc 15e cocc 16e cocc	Gln ttc Phe ggc Gly atc Ile Caa Gln 285 tgt	teces series at constant to the constant to th	ctgc ctgc atcc atcc atcc atca Ile 255 gacc Asp agai Arg	ctg ctg 240 ago Ser cag Cln tto Phe ctg Leu	Leu 225 ccc Pro Pro Phe Acc Asn Ser 305 gag	Glr cac His gcc Ala tcc Ser aca Thr 290 tac Tyr	xaa a atg aaaa Lys ctg 275 gtg Val	gct Ala gtc Val 260 Ctg Leu ttc Phe	1314 1362 1410 1458
W>	1011 103 104 105 107 108 109 111 112 113 115 116 117 119 120 121 123 124 125	gao Asp 245 atc 11e agg Lys aac Asn gaa Glu	cgac Argania Argania Met Caracteris Ser Gly Ala gac Asp 310	2155 cag Gln Ltca Gln Ltca Cag Gln Ltca Cag Gln Ltca Cag Gln Ltca Cag Cag Cag Cag Cag Cag Cag Cag Cag Ca	tagg Trp acc Thr ttc Phe gct Ala act Thr gca Ala	Gly Ggg Arg tacc Tyr aggg Arg Arg 265 ttc Gly gga Gly	aaaa Lys atg Met 250 gac Asp gag Glu acc Thr	gagger ga	Try 220 atc. 11ec aaaa aaaa bays Cocc Pro	o Glm tttc Phe ggc Gly atc Caa Gln Cys Caa Gln	cys: too: too: Ser atc. gagg Glu 270 ctg Gly ctt Leu	teu	ctgue ttcu	Leu 2259 coc Pro	Glr cac His gcc Ala cac Thr 290 tac Tyr	xaaa xaaa xaaa xaaa xaaa xaaa xaaa xaa	gct Ala gtc Val 260 ctg Leu ttc Phe ttg Leu ctg Leu	1314 1362 1410 1458 1506
	101 103 104 105 107 108 111 112 113 115 116 117 120 121 123 124 125 127	ago Ser gao Asp 245 ato Lie aag Lys aac Asm gaa Glu	c cga Arg 230 Met i tcc Ser ggg Gly Ala gac Asp 310 ttc	2155 cag Gln Load Load Load Load Load Load Load Load	Ala Ala	Gly Ggg Arg Arg Arg Arg Arg Arg Arg Arg Arg A	aaaa Lys atg Met 2500 Asp gag Glu acc Thr ggc Gly ctg	gagger ga	Try 220 1 atc 1 lee 2 aaa 2 Lys Pro 1 tgt 300 300 300 300 300 6 Glu	e Glm e ttcc e Phe e ggc e Gly e ttc e Gly e tgt caa e Gln cys caa e Gln ctg	cys: too: too: Ser atc.: gaggg Glu 270 ctg Leu ctt Leu cag	: Leu	ctglictgram ctglic	Leu 2259 coc Pro	Glr cac His cac His cac His cac His cac His cac Ala ca	A Xaa A taga A t	gct Ala gtc Val 260 ctg Leu ttc Phe ttg Leu tat	1314 1362 1410 1458
	101 103 104 105 107 108 111 112 113 115 116 117 121 123 124 125 127 128	ago Ser gao Asp 245 ato Lie aag Lys aac Glu aaa Lys	c cga Arg 230 Met c tcc c Ser ggg Ala gac Asp 310 ttc	2155 cag Gln Load Load Load Load Load Load Load Load	Ala Ala	Gly Ggg Arg Arg Arg Arg Arg Arg Arg Arg Arg A	aaaa Lys atg Met 2500 Asp gag Glu acc Thr ggc Cty Leu	gagger ga	Try 220 1 atc 1 lee 2 aaa 2 Lys Pro 1 tgt 300 300 300 300 300 6 Glu	e Glm e ttcc e Phe e ggc e Gly e ttc e Gly e tgt caa e Gln cys caa e Gln ctg	cys: too: too: Ser atc.: gaggg Glu 270 ctg Leu ctt Leu cag	: Leu	ctglictgram ctglic	Leu 2259 coc Pro	Glr cac His cac His cac His cac His cac His cac Ala ca	A Xaa A Atg A Met A Aaa A Lys C Ctg C Leu 275 Val C Cys C Cys A Atg A A A A	gct Ala gtc Val 260 ctg Leu ttc Phe ttg Leu tat Tyr	1314 1362 1410 1458 1506
	101 103 104 105 107 108 109 111 112 113 115 116 117 120 121 123 124 125 127 128	gao Asp 245 ato Lys ac Asp gaa Glu aaa Lys 325	c cyar 230 230 Met 1 too 2 Ser 2 gog Ala gac 310 tto	215 cag Gln	Ala tgg Trp acc Thr ttc Phe gct Ala act Thr	Gly Graph Grap	aaaa Lys atg Met 2500 gac Asp gag Glu acc Thr ggc Gly Ctg Leu 330	gagger ga	Try 220 atc 11e aaaa Lys ccc Pro tgt 300 cag cag Lys	caaa Gln ctg	ctt Cys ctcc ctcc ctcc ctcc ctcc ctcc ctcc ct	teu ctgurant	ctglictgram ctglic	Leu 225 ecc Pro Estate	Glr cac His gcc Ala cac Ser aca Thr 290 tac Pro	xaa atga atga atga atga atga atga atga a	gct Ala gtc Val 260 ctg Leu ttc Phe ctg Leu tat Tyr 340	1314 1362 1410 1458 1506



JAN 0 8 2001

TECH CENTER 1600/2900

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Output Set: N:\CRF3\01042001\I458366A.raw

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132 133	Val Le	u Met	Glņ	Ala 345	lle	Ser	Leu	Phe	Ser 350	Pro	Asp	Arg	Ьtó	Gly 355	Val	
135	ctq ca	q cac	ege	gtg	gtg	gac	cag	ctg	cag	gag	caa	ttc	gcc	att	act	1698
136	Leu Gl	n His	Arg	Val	٧al	Asp	Gln	Leu	Gln	Glu	Gln	Phe	Ala	Lle	Thr	
137			360			•		365					370			
	ctg aa	a tee	tac	att	qaa	tac	aat	caa	ccc	caq	cet	act	cat	aqq	ttc	1746
	Leu Ly															
141		375				-1 -	380	5				385		,		
	ttg tt			ate	ato	act		ete	acc	aaa	ete		age	atc	aat	1794
	Leu Pl	_	-			_							-			
145	39		10,10		.,,	395		2.50		0.14	400		00.2			
	get ca		200	cad	caa		cta	COC	ate	can		ata	cac	ccc	+++	1842
	Ala Gl	.,			** **			•								1012
	405	11 1113	. 3.11.1	0 1.11	410	neu	Lieu	ET 9	116	41.5	rat,	1. 1 €.	11 1.5	11.0	420	
		a 000	ata	ata		aaa	Etra	trt a	(1/1/1		202	aat	300		420	1884
	get ac															1004
153	Ala Th	L PIC	Leu	425	GIH	G.L.(I	Leu	rne	430	116	1111.	GLY	Ser			
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156	gcacto	cegg	geca	agac	ag a	tgga	cact	g cca	agag	geeg	acaa	atge	ect (getge	gectgt	2004
157	ctccct	aggg	aatt	cotg.	ct a	tgaca	ageto	g get	tagea	attc	ctca	aggaa	agg a	acate	ggggtg	2064
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1.61	<21.1>	LENGT	H: 4	34												
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1.68	<400>	SEQUE	NCE:	2												
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170	1			5	•				10			-		15		
1.71	Cys G1	u Asp	Thr	Glu	ser	Va.l	Pro	Glv	Lys	Pro	ser	Val.	Asn	Ala	Asp	
1.72			20					25	-				30		•	
	Glu Gl	u Val	Glv	Gľy	Pro	Gln	Ile	CVS	Ara	Va.L	Cvs	Glv	Asp	Lys	Ala	
174		35					40	-1	5		- 4 -	45	L	-, -		
	Thr Gl		His	Phe	Asn	Val		Thr	Cvs	Glu	GTV	CVS	Lvs	Glv	Phe	
1.76	50					55			• 1		60	-2.2				
	Phe Ar		Ala	Met	Lvs		Asn	Ala	Ara	Len		CVS	Pro	Phe	Ara	
178		9 -1.2.9	1114	1100	70				9	75	9	9,5			80	
	Lys Gl	o Ala	Cve	G) n		Thr	Δra	Lve	Thr		Ara	Gln	Cve	Gl n		
180	nys Gr	i ura	O _I 3	85	J 1 C.	1112	131.9	L.y.5	90	ru g	232.9	O i. ii	OJ S	95	712.0	
	Cys Ar	a Leu	Ara	LVS	Cvs	Len	Glu	Ser	Glv	Met	LVS	LVS	G1n	Met.	He	
182	J.5 111	,	100	2210	5,5		22.4	105	2	-1.50	-31 0		110			
	Met Se	r Asp		Ala	Val.	Glu	Glu		Arg	Ala	Leu	$_{\rm 11e}$	Lys	Arg	Lys	
1.84		1.15					120					125				
185	Lys Se	r Glu	Arg	Thr	Ġly	Thr	Gl.n	Pro	Leu	Gly	Val	Gln	G.1 y	Leu	Thr	
186	13					135				-	140					
187	Glu Gl	u Gln	Arq	Met	Met	Ile	Arg	Glu	Leu	Met	Asp	Ala	Cln	мet	Lys	
															160	

189 Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly

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JAN 0 8 2001

TECH CENTER 1500/2000

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                                                        175
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    194 195
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    196 210
                         21.5
                                              220
W--> 197 Leu Gln Xaa Pro Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu
    198 225
                230
                                         235
    199 Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser
    200 245 250
    201 Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
    202
                260
                               265
                                                   270
    203 Tie Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe
    204 275
                              280
                                                 285
    205 Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu
    206 290
                  295
                                             300
    207 Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu
    208 305
                 310
                                        31.5
                                                           320
    209 Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His
                    325
                              330
                                                        335
    211 Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp
    21.2 340
                          345
                                                  350
    213 Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln
    214 355
                       . 360
    215 Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro
    21.6 370 375
                                            380
    217 Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu
    218 385
                      390
                                        395
    219 Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
                                    410
                  405
                                                       4.15
    220
    221 Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr
    223 Glv Ser
    226 <210> SEQ ID NO: 3
    227 <211> LENGTH: 25
    228 <212> TYPE: DNA
    229 <213> ORGANTSM: Artificial Sequence
    231 <220> FEATURE:
    232 <223> OTHER INFORMATION: putative SXR response element from the steroid
           hydoxylase, rCYP3A1
    235 <400> SEQUENCE: 3
                                                                      25
    236 tagacagttc atgaagttca tetac
    238 <210> SEQ TD NO: 4
    239 <211> LENGTH: 25
    240 <212> TYPE: DNA
    241 <213> ORGANISM: Artificial Sequence
    243 <220> FEATURE:
    244 <223> OTHER INFORMATION: putative SXR response element from the steroid
```

RAW SEQUENCE LISTING DATE: 01/04/2001.
PATENT APPLICATION: US/09/458,366A TIME: 13:03:43

Input Set : A:\ES.txt

Output Set: N:\CRF3\01042001\1458366A.raw

```
245
          hydoxylase, rCYP3A2
247 <400> SEQUENCE: 4
                                                                            25
248 taagcagtto ataaagttoa totac
250 <210> SEO LD NO: 5
251 <211> LENGTH: 25
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: putative SXR response element from the steroid
257
          hydoxylase, rUGT1A6
259 <400> SEQUENCE: 5
                                                                            25
260 actitagete ataaagetea catig
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 26
264 <212> TYPE: DNA
265 <213> ORGANTSM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: putative SXR response element from the steroid
269
          hydoxylase, rbCYP2C1
271 <400> SEQUENCE: 6
272 caatcagttc aacagggttc accaat
                                                                            26
274 <210> SEQ TD NO: 7
275 <211> LENGTH: 33
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: putative SXR response element from the steroid
281
          hydoxylase, rP450R
283 <400> SEQUENCE: 7
284 cacaggtgag ctgaggccag cagcaggtcg aaa
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 27
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: putative SXR response element from the steroid
293
          hydoxylase, rCYP2A1
295 <400> SEQUENCE: 8
                                                                            27
296 gtgcaggttc aactggaggt caacatg
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 27
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: putative SXR response element from the steroid
          hydoxylase, rCYP2A2
307 <400> SEQUENCE: 9
                                                                           27
308 gtgctggttc aactggaggt cagtatg
310 <210> SEQ ID NO: 10
```



Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 01/04/2001

PATENT APPLICATION: US/09/458,366A

TIME: 13:03:44

Input Set : A:\ES.txt

Output Set: N:\CRF3\01042001\1458366A.raw

L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:197 M:258 W: Mandatory Feature missing, <221> not found for SEO ID#:2 L:197 M:258 W: Mandatory Feature missing, <222> not found for SEO ID#:2 L:197 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2 L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23